## The first description of a male of *Paraplectana sakaguchii* (Araneae: Araneidae)

# Akio Tanikawa<sup>1)</sup> & Tomoyuki Harigae<sup>2)</sup>

Laboratory of Biodiversity Science, School of Agriculture and Life Sciences, The University of Tokyo, 1–1–1, Yayoi,
Bunkyo-ku, Tokyo, 113–8657 Japan
E-mail: dp7a-tnkw@j.asahi-net.or.jp

2) 3–9–3, Nishi-oi, Shinagawa-ku, Tokyo, 140–0015 Japan
E-mail: kamonohasi.bird@orange.zero.jp

**Abstract** — A male of *Paraplectana sakaguchii* Uyemura 1938 is described for the first time using specimens obtained by rearing juvenile spiders. The morphological and molecular features are used for the identification of the specimens.

Key words — taxonomy, Paraplectana sakaguchii, male, DNA bar-coding

#### Introduction

The spider genus *Paraplectana* comprises 12 species described from Africa and Asia (Platnick 2010). The males of these spiders have never been described. Two species, *P. sakaguchii* Uyemura 1938 and *P. tsushimensis* Yamaguchi 1960, have been known to the Japanese fauna. They are rare and only several females have been found per year, making it difficult to find male spiders in the field.

Recently we obtained an unknown Cyrtarachnine egg-sac (Fig. 1), which seemed to be that of Paraplectana sakaguchii, Paraplectana tsushimensis, or Pasilobus hupingensis, because the egg-sacs of all the other Japanese species of Cyrtarachnine spiders have been already known. We reared the juvenile spiders emerged from the egg-sac in order to obtain adult specimens. Although we succeeded to obtain several adult male specimens, all of the females died before maturation. The morphological feature of young females resembled that of Paraplectana sakaguchii. Because we were not able to examine the female genital organ, we analyzed a partial sequence of mitochondrial cytochrome oxidase subunit I gene (mt-COI) to ensure the identification. As a result, we confirmed those specimens as P. sakaguchii by molecular features. Using those male specimens, we make a description of the male of P. sakaguchii for the first time in this paper.

The voucher specimens of this study are deposited in the collection of the department of zoology, National Museum of Nature and Science, Tokyo (NSMT). Nucleotide sequence data analyzed in this paper are available in the DDBJ/EMBL/GenBank databases.

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offering the egg-sac used in this study.

### **Identification of specimens**

*Morphology*. The abdomen of young female specimens were red and provided with many white spots on dorsum, and laterally with two pairs of black spots. These features agreed with the coloration and markings of *P. sakaguchii* (Yaginuma 1986; Chikuni 1989; Tanikawa 2007).

Molecular study. One juvenile specimen was used for molecular study. The specimen was preserved in 99.5% ethanol, and genomic DNA was extracted from whole cepharothorax using DNeasy Blood & Tissue kit (Qiagen, Inc.). The mt-CO1 partial sequence was amplified using the primer combination LCOI-1498: 5'-GGT CAA CAA ATC ATA AAG ATA TTG G-3' with HCOI-2198: 5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3' (Folmer et al. 1994). The reactants were initially denatured for 2 min at 95°C, proceeded with 40 cycles of 15 sec at 95°C, 20 sec at 47°C, 30 sec at 72°C. PCR product was purified using the ExoSAP-IT (GE Healthcare Bio-Sciences, Co. Ltd.). The purified PCR product was sequenced using the BigDye terminator cycle sequencing kit and analysed on ABI 3100 automated DNA sequencer (Applied Biosystems, Foster City, CA). Chromatogram was checked by eye. The obtained sequence was compared with those of allied species, especially the congener P. tsushimensis, in DDBJ/EMBL/ GenBank database (see appendix). Sequence alignments were done by Clustal W program (Thompson et al. 1994) in MEGA version 4.0 (Tamura et. al. 2007). The phylogenetic tree was constructed by Neighbor Joining method using MEGA version 4.0 (Tamura et al. 2007). The obtained unrooted NJ tree is shown in Fig. 2. The specimen in question made a well supported monophyletic clade with Parapletana sakaguchii. Its p-distance (the number of nucleotide difference divided by total number of nucleotides)

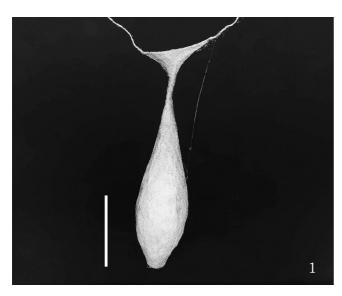
from *P. sakaguchii* was 0.014, while those from the two *P. tsushimensis* were 0.047 and 0.048.

Conclusion. We identified the specimens obtained as *Paraplectana sakaguchii* by the morphological and moleculer features: 1) the morphological features of young females agreed with those of *P. sakaguchii*, 2) the sequence data of mt-COI well agreed with that of *P. sakaguchii*.

### **Description**

Paraplectana sakaguchii Uyemura 1938 [Japanese name: Sakaguchi-torinofundamashi] (Figs. 1, 3-4)

Paraplectana sakaguchii Uyemura 1938, p.90, figs. 1a-b, pl. 7;



**Fig. 1.** Unknown egg-sac. Identified as *Paraplectana sakaguchii* in this study. (Scale: 10 mm.)

Yaginuma 1986, p.111, pl. 28, fig. 8; Chikuni 1989, p.83, fig. 63; Yin et al. 1997, p.385, figs. 277a-b; Song, Zhu & Chen 1999, p.302, figs. 181Q, 182C; Tanikawa 2007, p.10, 50, figs. 52-53, 461; Tanikawa 2009, p.428, fig. 49.

Specimens examined. 5♂, Hinode-machi, Nishi-tamagun, Tokyo, Japan, 15-VII-2009, K. Arai & R. Kono leg. (NSMT-Ar 8700-8704; collected as an egg-sac, became adult spiders after rearing.)

*Description.* Coloration and markings. Male (Fig. 2): carapace brown marginally dark brown; dorsum of abdomen yellow brown, with darker spots at sigilla.

Measurements (in mm). Based on specimen no. NSMT-Ar 8700, measurements in parentheses indicate the range among 5 specimens. Body 2.34 (2.20–2.34) long. Carapace 1.06 (1.01–1.08) long; 0.98 (0.92–0.98) wide. Length of legs [tarsus+metatarsus+tibia+patella+femur=total]: I, 0.31+0.55+0.65+0.41+1.00=2.92; II, 0.31+0.53+0.61+0.40+0.94=2.79; III, 0.26+0.34+0.39+0.28+0.66=1.93; IV, 0.25+0.38+0.50+0.34+0.79=2.26. Abdomen 1.45 (1.29–1.45) long; 1.68 (1.57–1.68) wide.

Male. Carapace slightly longer than wide [length divided by width 1.09 (1.09–1.16)]. Median ocular area wider than long [length divided by width 0.78 (0.57–0.86)]; wider in front than behind [anterior width divided by posterior width 1.18 (1.13–1.58)]. Labium slightly wider than long [length divided by width 0.77 (0.57–0.87)]. Sternum slightly wider than long [length divided by width 0.91 (0.81–1.00)]. Male palp (Fig. 3): embolus rostriform, median apophysis vent and thinning. Length of leg I divided by length of carapace 2.75 (2.69–2.84). Metatarsus and tibia of 1st and 2nd legs prolaterally with a low of weak spines. Abdomen wider than long [length divided by width 0.86 (0.82–0.86)], sigilla indistinct.

Distribution. Japan (Honshu, Shikoku, and Kyushu),

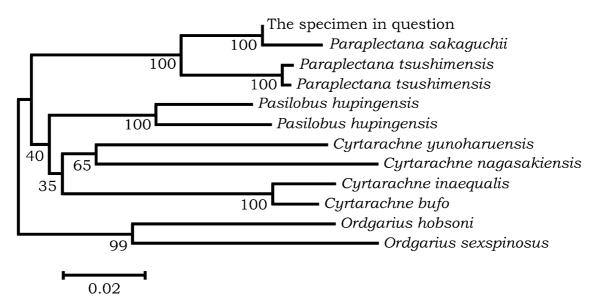
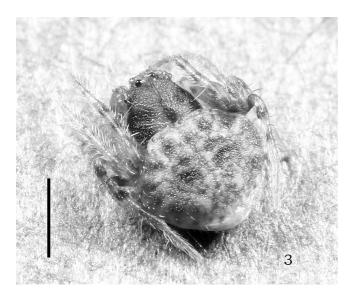
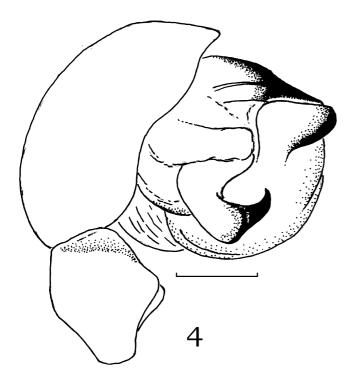


Fig. 2. Unrooted bootstrap consensus tree obtained by Neighbor Joining method for the species examined. Scores at each node are bootstrap values (1000 replicates). Scalebar shows substitution per site.



**Fig. 3.** Male of *Paraplectana sakaguchii* Uyemura 1938, when alive. (NSMT-Ar 8700; scale: 1 mm.)



**Fig. 4.** Male palp of *Paraplectana sakaguchii* Uyemura 1938, prolateral view. (NSMT-Ar 8700; scale: 0.1 mm.)

### China.

Remarks. The male of Paraplectana sakaguchii resembles those of Cyrtarachne spiders in general appearance. The rostriform embolus is a common feature among P. sakaguchii, C. bufo and C. inaequalis in contrast to the filiform embolus of C. nagasakiensis or C. yunoharuensis. The male of P. sakaguchii can be distinguished from C. inaequalis and bufo by the distally bent and flattened

median apophysis. The male of *Pasilpobus hupingensis* has a filiform embolus and a fishhook-shaped median apophysis. The male palps of *Ordgarius sexspinosus* and *O. hobsoni* can be distinguished from those of the above related spiders by having terminal apophysis.

The egg-sac of *Paraplectana sakaguchii* is fusiform and light brown as shown in Fig. 1. It resembles that of *P. tsushimensis* but can be distinguished by thinner upper part.

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**Appendix**. DDBJ/EMBL/GenBank accession numbers of sequence data analyzed in this study.

Species	Accession No.
The specimen in question	AB46976
Paraplectana sakaguchii	DQ518420
Paraplectana tsushimensis	DQ518422
Paraplectana tsushimensis	DQ518423
Pasilobus hupingensis	DQ518424
Pasilobus hupingensis	DQ518425
Cyrtarachne yunonaruensis	AB46975
Cyrtarachne nagasakiensis	DQ518414
Cyrtarachne inaequalis	DQ518415
Cyrtoarachne bufo	DQ518421
Ordgarius hobsoni	DQ518417
Ordgarius sexspinosus	DQ518418